



RAW SEQUENCE LISTING

DATE: 02/03/2003

PATENT APPLICATION: US/09/509,482B

TIME: 11:00:43

Input Set : D:\Seqlist.txt

Output Set: N:\CRF4\02032003\I509482B.raw

4 <110> APPLICANT: Crofts, Linda Anne
5 Hancock, Manuela S.
6 Morrison, Nigel A.
7 Eisman, John A.
9 <120> TITLE OF INVENTION: Isoforms of the Human Vitamin D Receptor
12 <130> FILE REFERENCE: RICE-014
14 <140> CURRENT APPLICATION NUMBER: 09/509,482B
15 <141> CURRENT FILING DATE: 2000-09-15
17 <150> PRIOR APPLICATION NUMBER: PCT/AU98/00817
18 <151> PRIOR FILING DATE: 1998-09-29
20 <150> PRIOR APPLICATION NUMBER: P09500
21 <151> PRIOR FILING DATE: 1997-09-29
23 <160> NUMBER OF SEQ ID NOS: 20
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30 <213> ORGANISM: Homo sapiens
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51 ggcccaagct gtctgaggag cagcagcgca tcattggcatt actgctggac gccaccata 600
52 agacctacga ccccaacctac tccgacttct gccagtccg gcctccagtt cgtgtgaatg 660
53 atggtggagg gacccatcct tccaggccca actccagaca cactcccagc ttctctgggg 720
54 actcctcctc ctccctgctc gatcactgta tcacctcttc agacatgatg gactcgtcca 780
55 gcttctccaa tctggatctg agtgaagaag attcagatga cccttctgtg accctagagc 840
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59 tggacgacat gtcctggacc tgtggcaacc aagactacaa gtaccgcgtc agtgacgtga 1080
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61 agaagctgaa cttgcatgag gaggagcatg tcctgctcat ggccatctgc atcgtctccc 1200
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64 ccaagatgat ccagaagcta gccgacctgc gcagcctcaa tgaggagcac tccaagcagt 1380
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76 ctccctgcc tgaccctgga gactttgacc ggaacgtgcc ccgcatctgt ggggtgtgtg 180
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101 <212> TYPE: DNA

102 <213> ORGANISM: Homo sapiens

104 <400> SEQUENCE: 4

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107 ctccctgcc tgaccctgga gactttgacc ggaacgtgcc ccgcatctgt ggggtgtgtg 180
108 gagaccgagc cactggcttt cacttcaatg ctatgacctg tgaaggctgc aaaggcttct 240
109 tcagggtgagc cccctccca ggctctcccc agtggaagg gagggagaag aagcaagggtg 300
110 tttccatgaa gggagccctt gcatttttca catctccttc cttacaatgt ccatggaaca 360
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112 attcacctgc cccttcaacg gggactgccg catcaccaag gacaaccgac gccactgcca 480
113 ggcctgccgg ctcaaacgct gtgtggacat cggcattgat aaggagttca ttctgacaga 540
114 tgaggaagtg cagaggaagc gggagatgat cctgaagcgg aaggaggagg aggccttgaa 600
115 ggacagtctg cgGCCcaagc tgtctgagga gcagcagcgc atcattgcca tactgctgga 660
116 cgccaccat aagacctacg accccacctt ctccgacttc tgccagttcc ggcctccagt 720
117 tcgtgtgaat gatggtggag ggagccatcc ttccaggccc aactccagac acactccag 780
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124 cagtgcgtg accaaagccg gacacagcct ggagctgatt gagccctca tcaagttcca 1200
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126 catcgtctcc ccagatcgtc ctggggtgca ggacgccgcg ctgattgagg ccatccagga 1320
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128 cctgctctat gccaaagatga tccagaagct agccgacctg cgcagcctca atgaggagca 1440
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169 gggagatgat cctgaagcgg aaggaggagg aggccttgaa ggacagtctg cggcccaagc 660
170 tgtctgagga gcagcagcgc atcattgccg tactgctgga cgccaccat aagacctacg 720
171 accccacctg ctccgacttc tgccagttcc ggccctccagt tcgtgtgaat gatggtggag 780
172 ggagccatcc ttccaggccc aactccagac acactcccag cttctctggg gactcctcct 840
173 cctcctgctc agatcactgt atcacctctt cagacatgat ggactcgtcc agcttctcca 900
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183 tccagaagct agccgacctg cgcagcctca atgaggagca ctccaagcag taccgctgcc 1500
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207 Pro His Arg Arg Ala Pro Leu Gly Ser Thr Tyr Leu Pro Pro Ala Pro
208 35 40 45
209 Ser Gly Met Glu Ala Met Ala Ala Ser Thr Ser Leu Pro Asp Pro Gly
210 50 55 60
211 Asp Phe Asp Arg Asn Val Pro Arg Ile Cys Gly Val Cys Gly Asp Arg
212 65 70 75 80
213 Ala Thr Gly Phe His Phe Asn Ala Met Thr Cys Glu Gly Cys Lys Gly
214 85 90 95
215 Phe Phe Arg Arg Ser Met Lys Arg Lys Ala Leu Phe Thr Cys Pro Phe
216 100 105 110
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218 115 120 125
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224      165      170      175
225 Glu Gln Gln Arg Ile Ile Ala Ile Leu Leu Asp Ala His His Lys Thr
226      180      185      190
227 Tyr Asp Pro Thr Tyr Ser Asp Phe Cys Gln Phe Arg Pro Pro Val Arg
228      195      200      205
229 Val Asn Asp Gly Gly Gly Ser His Pro Ser Arg Pro Asn Ser Arg His
230      210      215      220
231 Thr Pro Ser Phe Ser Gly Asp Ser Ser Ser Ser Cys Ser Asp His Cys
232 225      230      235      240
233 Ile Thr Ser Ser Asp Met Met Asp Ser Ser Ser Phe Ser Asn Leu Asp
234      245      250      255
235 Leu Ser Glu Glu Asp Ser Asp Asp Pro Ser Val Thr Leu Glu Leu Ser
236      260      265      270
237 Gln Leu Ser Met Leu Pro His Leu Ala Asp Leu Val Ser Tyr Ser Ile
238      275      280      285
239 Gln Lys Val Ile Gly Phe Ala Lys Met Ile Pro Gly Phe Arg Asp Leu
240      290      295      300
241 Thr Ser Glu Asp Gln Ile Val Leu Leu Lys Ser Ser Ala Ile Glu Val
242 305      310      315      320
243 Ile Met Leu Arg Ser Asn Glu Ser Phe Thr Met Asp Asp Met Ser Trp
244      325      330      335
245 Thr Cys Gly Asn Gln Asp Tyr Lys Tyr Arg Val Ser Asp Val Thr Lys
246      340      345      350
247 Ala Gly His Ser Leu Glu Leu Ile Glu Pro Leu Ile Lys Phe Gln Val
248      355      360      365
249 Gly Leu Lys Lys Leu Asn Leu His Glu Glu Glu His Val Leu Leu Met
250      370      375      380
251 Ala Ile Cys Ile Val Ser Pro Asp Arg Pro Gly Val Gln Asp Ala Ala
252 385      390      395      400
253 Leu Ile Glu Ala Ile Gln Asp Arg Leu Ser Asn Thr Leu Gln Thr Tyr
254      405      410      415
255 Ile Arg Cys Arg His Pro Pro Pro Gly Ser His Leu Leu Tyr Ala Lys
256      420      425      430
257 Met Ile Gln Lys Leu Ala Asp Leu Arg Ser Leu Asn Glu Glu His Ser
258      435      440      445
259 Lys Gln Tyr Arg Cys Leu Ser Phe Gln Pro Glu Cys Ser Met Lys Leu
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VERIFICATION SUMMARY

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